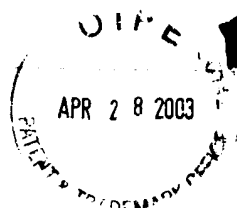


SEQUENCE LISTING



0110: Massague et al.

0120: ISOLATED p27 PROTEIN AND METHODS FOR ITS PRODUCTION AND USE

0130: GPCI-P08-079

0140: 09/865018

0141: 2001-05-24

0150: 08/854039

0151: 1997-05-09

0160: 27

0170: PatentIn version 3.1

0210: 1

0211: 597

0212: DNA

0213: Homo sapiens

0220:

0221: CDS

0222: (1..1597)

0223:

0400: 1

atg tca aac atg cga gtg tct aac ggg agc cct agc ctg gag cgg atg	48
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Asp Ala Arg Gln Ala Glu His Pro Lys Pro Ser Ala Cys Arg Asn Leu	
20 25 30	

tgc gcc cgg atg gac cac gaa gac tta acc cgg gac ttg gag aag cac	144
Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His	
35 40 45	

ttc cga gac atg gaa gag ggc agc cag ccc aag tgg aat ttc gat ttc	192
Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe	
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cag cat cac aaa ccc cta gag ggt aag tac gag tgg cca gag gtg gag	240
Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu	
65 70 75 80	

aag gcc acc ttg ccc gag ttc tac tac aga ccc cgg cgg ccc ccc aaa	288
Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys	
85 90 95	

ggc gcc tgc aag atg cgg ggc cag gag agc cag gat gtc agc ggg agc	336
Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser	
100 105 110	

cgc cgg ggc ggc cct tta att ggc gct cgg gct aac tct gag gac acg	384
Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr	

115	120	125	
cat ttg gtg gac cca aag act gat ccg tgg gac agc bag acg ggg tta			432
His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu			
130	135	140	
ggg gag caa tgc gca gga ata agg aag cga cct gca acc gac gat tct			480
Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser			
145	150	155	160
tct act caa aac aaa aga gcc aac aga aca gaa gaa aat gtt tca gac			528
Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp			
165	170	175	
ggt tcc cca aat gcc ggt tct gtg gag bag acg ccc aag aag cct gcc			576
Gly Ser Pro Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly			
180	185	190	
ctc aga aga cgt caa acg taa			597
Leu Arg Arg Arg Gln Thr			
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Phe Gly Pro Val Asp His Glu Gln Leu Thr Arg Asp Leu Glu Lys His			
35	40	45	
Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe			
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Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu			
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Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys			
85	90	95	
Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser			
100	105	110	
Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr			
115	120	125	

His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu
130 135 140

Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
145 150 155 160

Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
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180 185 190

Leu Arg Arg Arg Gln Thr
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1 5 10 15
gac gcc aga cca gcc gat cac ccc aag cct tcc gcc tgc aga aat ctc 96
Asp Ala Arg Gln Ala Asp His Pro Lys Pro Ser Ala Cys Arg Asn Leu
20 25 30
ttc ggc cgg gtc aat cat gaa gaa cta acc cgg gac ttg gag aag cac 144
Phe Gly Pro Val Asn His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
35 40 45
ttc cgg gat arg gaa gaa gcc agt cag cgc aag tgg aat ttc gac ttt 192
Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
50 55 60
cag aat cat aag ccc ctg gag gcc aga tac gaa tgg cag gag gtg gag 240
Gln Asn His Lys Pro Leu Glu Gly Arg Tyr Glu Trp Gln Glu Val Glu
65 70 75 80
cag ggc agc ttc ccc gag ttc tac tac agc ccc cgg cgc ccc ccc aag 288
Arg Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
85 90 95
aac gcc tgc aac gtg ctg gcc cag gag agc cag gat gtc agc ggc agc 336
Ser Ala Cys Lys Val Leu Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
100 105 110
cgc cag gcc gtg cct tta att ggg tct cag gca aac tct gag gac cgg 384

Arg Gln Ala Val Pro Leu Ile Gly Ser Gln Ala Asn Ser Glu Asp Arg
 115 120 125
 cat ttg gtg gac caa atg cct gac tgg tca gac aat cag gct ggg tta 432
 His Leu Val Asp Gln Met Pro Asp Ser Ser Asp Asn Gln Ala Gly Leu
 130 135 140
 gag gag cag tgt cca ggg atg agg aag cga cct gct gca gaa gat tct 480
 Ala Glu Gln Cys Pro Gly Met Arg Lys Arg Pro Ala Ala Glu Asp Ser
 145 150 155 160
 tct tgg caa aac aaa agg gcc aac aga aca gaa gaa aat gtt tca gac 528
 Ser Ser Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
 165 170 175
 ggt tcc ccg aac gct ggc act gta gag cag acg ccc aag aag ccc ggc 576
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 Leu Arg Arg Gln Thr
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 Phe Gly Pro Val Asn His Glu Gln Leu Thr Arg Asp Leu Glu Lys His
 35 40 45
 Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
 50 55 60
 Gln Asn His Lys Pro Leu Glu Gly Arg Tyr Glu Trp Gln Glu Val Glu
 65 70 75 80
 Arg Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
 85 90 95
 Ser Ala Cys Lys Val Leu Ala Gln Glu Ser Gln Asp Val Ser Gly Ser
 100 105 110
 Arg Gln Ala Val Pro Leu Ile Gly Ser Gln Ala Asn Ser Glu Asp Arg
 115 120 125

His Leu Val Asp Gln Met Pro Asp Ser Ser Asp Asn Gln Ala Gly Leu
 130 135 140

Ala Glu Gln Cys Pro Gly Met Arg Lys Arg Pro Ala Ala Glu Asp Ser
 145 150 155 160

Ser Ser Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
 165 170 175

Gly Ser Pro Asn Ala Gly Thr Val Glu Gln Thr Pro Lys Lys Pro Gly
 180 185 190

Leu Arg Arg Gln Thr
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<110>
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 Asp Ala Arg Gln Ala Glu Tyr Pro Lys Pro Ser Ala Cys Arg Asn Leu
 20 25 30

tcc ggc cgg gtc aac cac gaa gag ctg acc cgg gac ttg gag aag cac 144
 Phe Gly Pro Val Asn His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
 35 40 45

acc aga gac atg gaa gag gca agc cag cgc aag tgg aac ttt gat ttc 192
 Arg Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
 50 55 60

tat aat cac aag ccc ctg gag ggc aaa tac gag tgg cag gag gtg gag 240
 Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
 65 70 75 80

aag ggc agc ttg cgg gag ttc tac tac aga ccc cgg cgg cca ccc aaa 288
 Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
 85 90 95

ggc gcc tgc aag gtg cgg ggg cag gag acc cag gac gtc agc ggg acc 336
 Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Thr
 100 105 110

cgg cag gcc gtg cct tta atg ggg tct cag gca aac tca gag gac aca 384
 Arg Gln Ala Val Pro Leu Met Gly Ser Gln Ala Asn Ser Glu Asp Thr
 115 120 125

cac atg gta gag caa aag act gag aag ggg gac aac cag gct ggc tta 432
 His Leu Val Asp Gln Lys Thr Asp Thr Ala Asp Asn Gln Ala Gly Leu
 130 135 140

ggg gag cag tgc act ggg atc agg aag cga ccg gcc aca gac gat tcc 480
 Ala Glu Gln Cys Thr Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
 145 150 155 160

tct cct caa aac aaa aga gcc aac aga aca gaa gaa aat gtc tca gag 528
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 165 170 175

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 Gly Ser

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Phe Gly Pro Val Asn His Glu Glu Leu Thr Arg Asp Leu Glu Lys His
 35 40 45

Arg Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe
 50 55 60

Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu
 65 70 75 80

Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys
 85 90 95

Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Thr
 100 105 110

Arg Gln Ala Val Pro Leu Met Gly Ser Gln Ala Asn Ser Glu Asp Thr
 115 120 125

His Leu Val Asp Gln Lys Thr Asp Thr Ala Asp Asn Gln Ala Gly Leu

130

135

140

Ala Glu Gln Cys Thr Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser
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Ser Pro Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp
 165 170 175

Gly Ser

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<21> 15

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<220> 19

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<211> 20
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<214>
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<400> 2
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<211> 1
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Leu Ser Gln Pro Val Asn

1 5

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<400> 34

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Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg
 35 40 45

Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala
 50 55 60

Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr
 65 70 75 80

Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg Arg Pro Gly
 85 90 95

Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp
 100 105 110

Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu
 115 120 125

Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln
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Lys Arg Lys Pro

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